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ORIGINAL ARTICLE

Oceanographic connectivity and environmental correlates of genetic structuring in Atlantic herring in the Baltic Sea

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Abstract

Marine fish often show little genetic structuring in neutral marker genes, and Atlantic herring (Clupea harengus) in the Baltic Sea are no exception; historically, very low levels of population differentiation (F_{ST} 0.002) have been found, despite a high degree of interpopulation environmental heterogeneity in salinity and temperature. Recent exome sequencing and SNP studies have however shown that many loci are under selection in this system. Here, we combined population genetic analyses of a large number of transcriptome-derived microsatellite markers with oceanographic modelling to investigate genetic differentiation and connectivity in Atlantic herring at a relatively fine scale within the Baltic Sea. We found evidence for weak but robust and significant genetic structuring (F_{ST} = 0.008) explainable by oceanographic connectivity. Genetic differentiation was also associated with site differences in temperature and salinity, with the result driven by the locus Her14 which appears to be under directional selection (F_{ST} = 0.08). The results show that Baltic herring are genetically structured within the Baltic Sea, and highlight the role of oceanography and environmental factors in explaining this structuring. The results also have implications for the management of herring fisheries, the most economically important fishery in the Baltic Sea, suggesting that the current fisheries management units may be in need of revision.

Introduction

Intraspecific biodiversity forms the basis for evolution and is important for the long-term viability of populations and thereby also for sustainable harvesting of species of commercial importance (Frankham et al. 2002; Avise 2008; Schindler et al. 2010). Hence, a better understanding of the factors shaping intraspecific biodiversity is one of the key goals in evolutionary and conservation biology (Allendorf and Luikart 2007).

In the marine environment, gene flow by drifting larvae and migrating adults may be extensive, and accordingly, local adaptation in marine fish has traditionally been viewed as rare, with weak population structuring (Waples 1998). However, recent studies show that marine fish may be spatially structured into genetically distinct populations on both wide (e.g. Bradbury et al. 2010) and remarkably fine geographic scales (e.g. Knutsen et al. 2011). Concurrent variation in ecologically important traits (e.g. spawning time, migration patterns etc.) among populations may also indicate adaptive differentiation, possibly 8ping intraspec4646009.n,(